SEQUENCE LISTING

<110> Lindsvogel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827
<151> 2000-08-08

<150> US 60/250,876
<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 2831
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (34)...(1755)

<400> 1

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tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc      54
                                     Met Arg Thr Leu Leu Thr Ile
                                      1               5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat      102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
         10                  15                  20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg      150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
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     25                  30                  35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc      198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
 40                  45                  50                  55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt      246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
                 60                  65                  70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac      294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
             75                  80                  85

ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc      342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
         90                  95                 100

cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act      390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr
     105                 110                 115

acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att      438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
120                 125                 130                 135

cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc      486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly
                140                 145                 150

cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta      534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu
            155                 160                 165

gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag      582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln
        170                 175                 180

aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc      630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly
    185                 190                 195

acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac      678
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Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr
200                 205                 210                 215

atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc      726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe
                220                 225                 230

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc      774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys
            235                 240                 245

tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc      822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser
        250                 255                 260

ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag      870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln
    265                 270                 275

gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg      918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu
280                 285                 290                 295

gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag      966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu
                300                 305                 310

ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta     1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu
            315                 320                 325

ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc     1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro
        330                 335                 340

cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc     1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val
    345                 350                 355

ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca     1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro
360                 365                 370                 375
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ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc      1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
                380                 385                 390

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg      1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
            395                 400                 405

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa      1302
Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
        410                 415                 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc      1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
    425                 430                 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg      1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
440                 445                 450                 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc      1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
                460                 465                 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg      1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
            475                 480                 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag      1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
        490                 495                 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca      1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
    505                 510                 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc      1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
520                 525                 530                 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca      1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
                540                 545                 550
```

```
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc      1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
            555                 560                 565

ctg act gtg cag tgg gag tcc tgagggaat gggaaaggct tggtgcttcc        1785
Leu Thr Val Gln Trp Glu Ser
        570

tccctgtccc tacccagtgt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca   1845
cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag   1905
ggcccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg   1965
gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag   2025
aaatgacagt gcaaggagga aatgcaggga aactcccgag gtccagagcc ccacctccta   2085
acaccatgga ttcaaagtgc tcagggaatt tgcctctcct tgccccattc ctggccagtt   2145
tcacaatcta gctcgacaga gcatgaggcc cctgcctctt ctgtcattgt tcaaaggtgg   2205
gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc   2265
agaacaacct gcacttctgc caaggccagg gccagcagga cggcaggact ctagggaggg   2325
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cattcctctg atagaacaaa gcgaaatgca ggtccaccag ggagggagac acacaagcct   2445
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gctgtggccc ctggacgggt acaataacac actgtactga tgtcacaact ttgcaagctc   2565
tgccttgggt tcagcccatc tgggctcaaa ttccagcctc accactcaca agctgtgtga   2625
cttcaaacaa atgaaatcag tgcccagaac ctcggtttcc tcatctgtaa tgtggggatc   2685
ataacaccta cctcatggag ttgtggtgaa gatgaaatga agtcatgtct ttaaagtgct   2745
taatagtgcc tggtacatgg gcagtgccca ataaacggta gctatttaaa aaaaaaaaaa   2805
aaaaaaaaaa atagcggccg cctcga                                        2831
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<210> 2
<211> 574
<212> PRT
<213> Homo sapien

<400> 2

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 1               5                  10                  15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
```

65 70 75 80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
85 90 95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
100 105 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
115 120 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
130 135 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145 150 155 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
165 170 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
180 185 190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
195 200 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
210 215 220
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
225 230 235 240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
245 250 255
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
260 265 270
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
275 280 285
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
290 295 300
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
305 310 315 320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
325 330 335
Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
340 345 350
Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
355 360 365
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
370 375 380
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
385 390 395 400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
405 410 415

```
Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
                420                 425                 430
Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
        435                 440                 445
Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
    450                 455                 460
His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
465                 470                 475                 480
Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
                485                 490                 495
Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
            500                 505                 510
Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
        515                 520                 525
Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
    530                 535                 540
Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
545                 550                 555                 560
Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
                565                 570
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<210> 3
<211> 211
<212> PRT
<213> Homo sapiens

<400> 3

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Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1               5                  10                  15
Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
        35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
                85                  90                  95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
            100                 105                 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
        115                 120                 125
```

```
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
    130                 135                 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145                 150                 155                 160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
                165                 170                 175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
            180                 185                 190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
        195                 200                 205
Thr Trp Thr
    210
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<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu peptide tag

<400> 4

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Glu Tyr Met Pro Met Glu
 1               5
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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag-tag peptide

<400> 5

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Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5
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<210> 6
<211> 699
<212> DNA
<213> Homo sapiens

<400> 6

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gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag      60
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg     120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc     180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag     240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc     360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg     420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc     600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     660
tacacgcaga agagcctctc cctgtctccg ggtaaataa                            699
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<210> 7
<211> 1116
<212> DNA
<213> homo sapiens

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<221> CDS
<222> (21)...(557)

<400> 7

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                       Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe
                         1               5                  10

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg      101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
            15                  20                  25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac      149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
        30                  35                  40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg      197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
    45                  50                  55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att      245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
60                  65                  70                  75
```

```
ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg      293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
                 80                  85                  90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa      341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
             95                 100                 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc      389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
         110                 115                 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg      437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
     125                 130                 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt      485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140                 145                 150                 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt      533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
                160                 165                 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac      587
Met Ser Leu Arg Asn Ala Cys Ile
            175

taacccccct tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca     647
aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt     707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag     767
catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt     827
atttttaaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa     887
aaacccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat     947
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa    1007
acatcattcg atattgctac ttgagtgtaa ggctaatatt gatatttatg acaataatta    1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta                1116
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<210> 8
<211> 179
<212> PRT
<213> homo sapiens

<400> 8

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
1 5 10 15
Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
20 25 30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
35 40 45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50 55 60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65 70 75 80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
85 90 95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100 105 110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115 120 125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130 135 140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145 150 155 160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
165 170 175
Ala Cys Ile

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC28590

<400> 9
ttgggtacct ctgcaatggc cgccctgcag aaatct 36

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC28580

<400> 10
ttgggatcca atgcaggcat ttctcagaga cat 33

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC14666

<400> 11
agccaccaag atgactga 18

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC14742

<400> 12
tgcatttggt aggtgcggtt ga 22

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 13
His His His His His His
1 5

<210> 14
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29239

<400> 14
gaggccggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 15
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29232

<400> 15
cgactgactc gagtcagtga tggtgatggt gatggccacc tgatccttta cccggagaca 60
gggag 65

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39319

<400> 16
atcggaattc gcagaagcca tggcgtggag ccttggg 37

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39325

<400> 17
cagtggatcc ggaggggacc gtttcgtc 28

<210> 18

<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(660)

<400> 18

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atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca      48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt      96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg     144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat     192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc     240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag     288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att     336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat     384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act     432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
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```
    130                 135                 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa      480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag      528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga      576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc      624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc                      660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220
```

<210> 19
<211> 220
<212> PRT
<213> Homo sapiens

<400> 19

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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110
```

```
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220
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<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC38931

<400> 20
acaaagccgc gggaggag 18

<210> 21
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39042

<400> 21
ctgactcgag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca 60
gtttacccgg agacagggag ag 82

<210> 22
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused to IgGg1 with a 6-HIS tag

<400> 22

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atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca      48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt      96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg     144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat     192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc     240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag     288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att     336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat     384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act     432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
```

```
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa      480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag      528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga      576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc      624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg      672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
    210                 215                 220

ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca      720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240

ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc      768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc      816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc      864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        275                 280                 285

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg      912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    290                 295                 300

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc      960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
```

```
305                 310                 315                 320

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc      1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                325                 330                 335

tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc      1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg      1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
        355                 360                 365

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc      1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    370                 375                 380

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg      1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385                 390                 395                 400

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc      1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405                 410                 415

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag      1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420                 425                 430

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac      1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt      1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
    450                 455                 460

ggt tcc gga tca ggt ggc cat cac cat cac cat cac                      1428
Gly Ser Gly Ser Gly Gly His His His His His His
465                 470                 475
```

<210> 23
<211> 476
<212> PRT
<213> Homo sapiens

<400> 23

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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Glu Tyr Trp Lys
145                 150                 155                 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
    210                 215                 220
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        275                 280                 285
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
```

```
    290                 295                 300
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305                 310                 315                 320
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                325                 330                 335
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
        355                 360                 365
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    370                 375                 380
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385                 390                 395                 400
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405                 410                 415
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420                 425                 430
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
    450                 455                 460
Gly Ser Gly Ser Gly Gly His His His His His His
465                 470                 475
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<210> 24
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29328

<400> 24
tcagaggaat cggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 25
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29231

<400> 25
cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60
gggag 65

<210> 26
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39335

<400> 26
atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC28981

<400> 27
tttgggctcc ctgagctctg gtggaa 26

<210> 28
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39043

<400> 28
ctgactcgag ctactccata ggcatatact cgccacctga tccggaacca cgcggaacca 60
gtttacccgg agacagggag 80

<210> 29
<211> 1452
<212> DNA

<213> Artificial Sequence

<220>
<223> h.cytorll extracellular cytokine binding domain
fused to IgGgl with a Glu-Glu tag

<221> CDS
<222> (1)...(1452)

<400> 29

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atg agg acg ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac      48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1               5                  10                  15

gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg aaa ttc cag tcc      96
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30

agc aac ttt gaa aac atc ctg acg tgg gac agc ggg cca gag ggc acc     144
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45

cca gac acg gtc tac agc atc gag tat aag acg tac gga gag agg gac     192
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60

tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg aag tcc tgc aac     240
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80

ctg acg gtg gag acg ggc aac ctc acg gag ctc tac tat gcc agg gtc     288
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95

acc gct gtc agt gcg gga ggc cgg tca gcc acc aag atg act gac agg     336
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110

ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt     384
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125

atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg     432
```

```
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140

cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc      480
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160

cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa      528
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175

atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc      576
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190

cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg      624
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205

gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac      672
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220

cgg aca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca      720
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240

tca gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag      768
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255

ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      816
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc      864
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag      912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300
```

```
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg      960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat     1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc     1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag     1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365

gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc     1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg     1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct     1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc     1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg     1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg     1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc ggt tca ggt ggc gag tat     1440
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480
```

atg cct atg gag 1452
Met Pro Met Glu

<210> 30
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> hzcytor11 extracellular cytokine binding domain fused to IgGg1 with a Glu-Glu tag

<400> 30

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Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1               5                  10                  15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
```

```
    210                 215                 220
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480
Met Pro Met Glu
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<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37693

<400> 31
ccccagacac gatctacagc at 22

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37449

<400> 32
gggtcaggcc gaagaactca tat 23

<210> 33
<211> 199
<212> PRT
<213> Homo sapiens

<400> 33

Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys
1				5					10					15	
Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
			20					25					30		
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
		35					40					45			
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
	50					55					60				
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65				70					75					80	
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
			85					90					95		
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
		100					105					110			
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
	115					120					125				
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
130					135					140					
Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	Val	Leu	Arg
145				150					155					160	
Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	Gly	Phe	Leu
			165					170					175		

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
180 185 190
Thr Thr His Asp Glu Thr Val
195

<210> 34
<211> 211
<212> PRT
<213> Homo sapiens

<400> 34
Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
1 5 10 15
Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
20 25 30
Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
35 40 45
Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
50 55 60
Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
65 70 75 80
Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
85 90 95
Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
100 105 110
Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
115 120 125
Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
130 135 140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145 150 155 160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
165 170 175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
180 185 190
Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
195 200 205
Thr Arg Gln
210

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<213> Homo sapiens

<400> 35

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 1               5                  10                  15
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
            20                  25                  30
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
        35                  40                  45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
    50                  55                  60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65                  70                  75                  80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
                85                  90                  95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
            100                 105                 110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
        115                 120                 125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
    130                 135                 140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145                 150                 155                 160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
                165                 170                 175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
            180                 185                 190
Glu Cys Val Glu Val Gln Gly Glu Ala
        195                 200
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